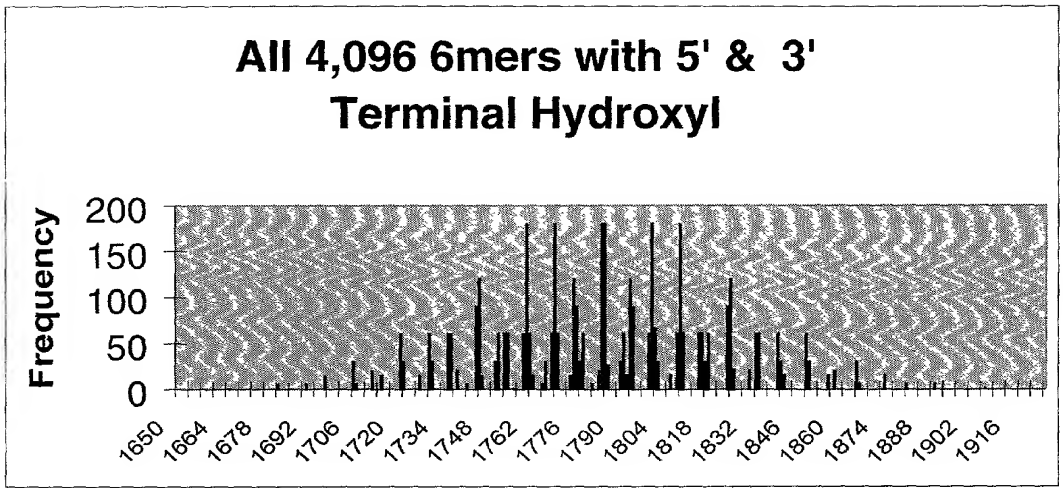
Figure 1


All 4,096 6mers with 5' & 3' Terminal Hydroxyl
Frequency
200
150
100
50
0
1650
1664
1678
1692
1706
1720
1734
1748
1762
1776
1790
1804
1818
1832
1846
1860
1874
1888
1902
1916

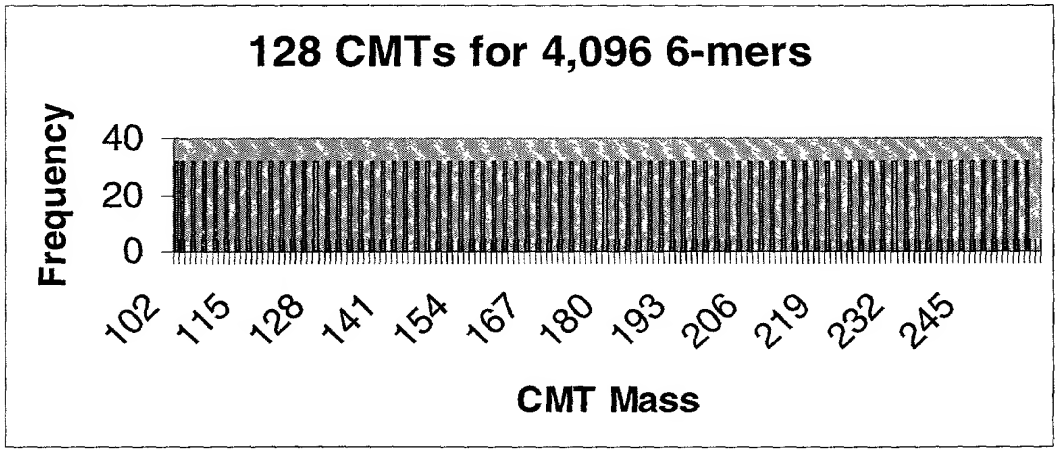
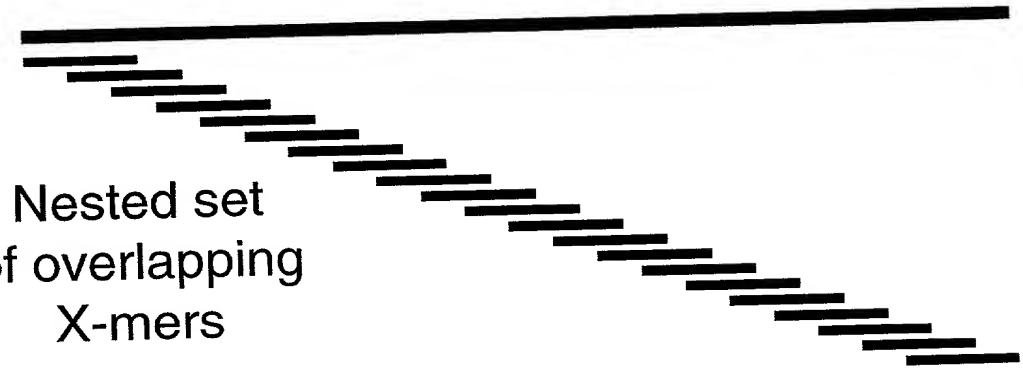
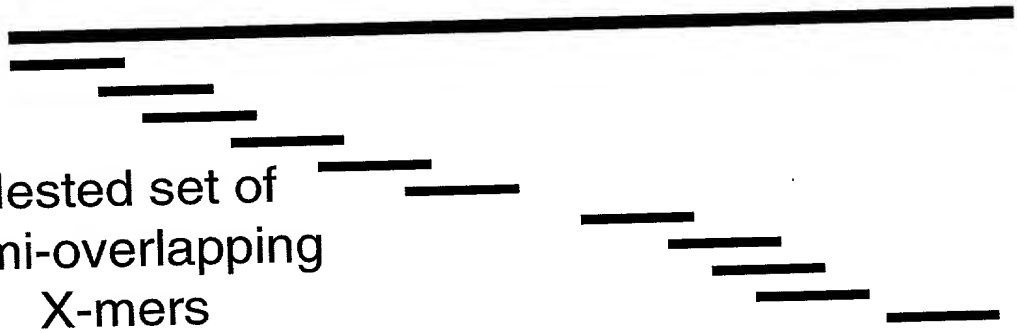

128 CMTs for 4,096 6-mers
Frequency
40
20
0
102
115
128
141
154
167
180
193
206
219
232
245
CMT Mass

Figure 2A



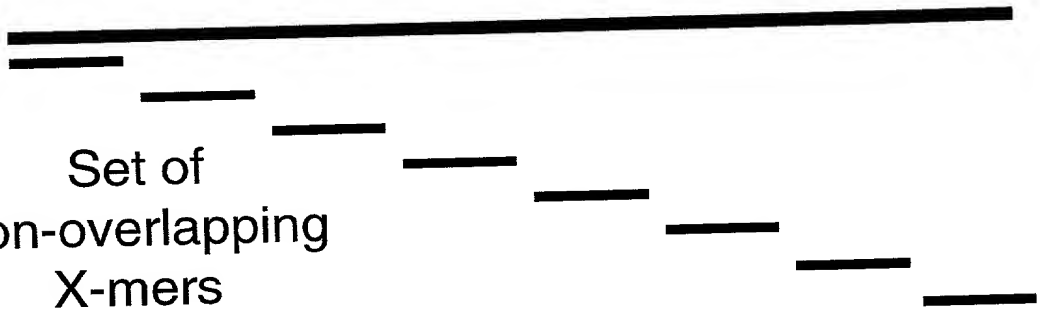
Nested set
of overlapping
X-mers

Figure 2B



Nested set of
semi-overlapping
X-mers

Figure 2C



Set of
Non-overlapping
X-mers

Figure 3

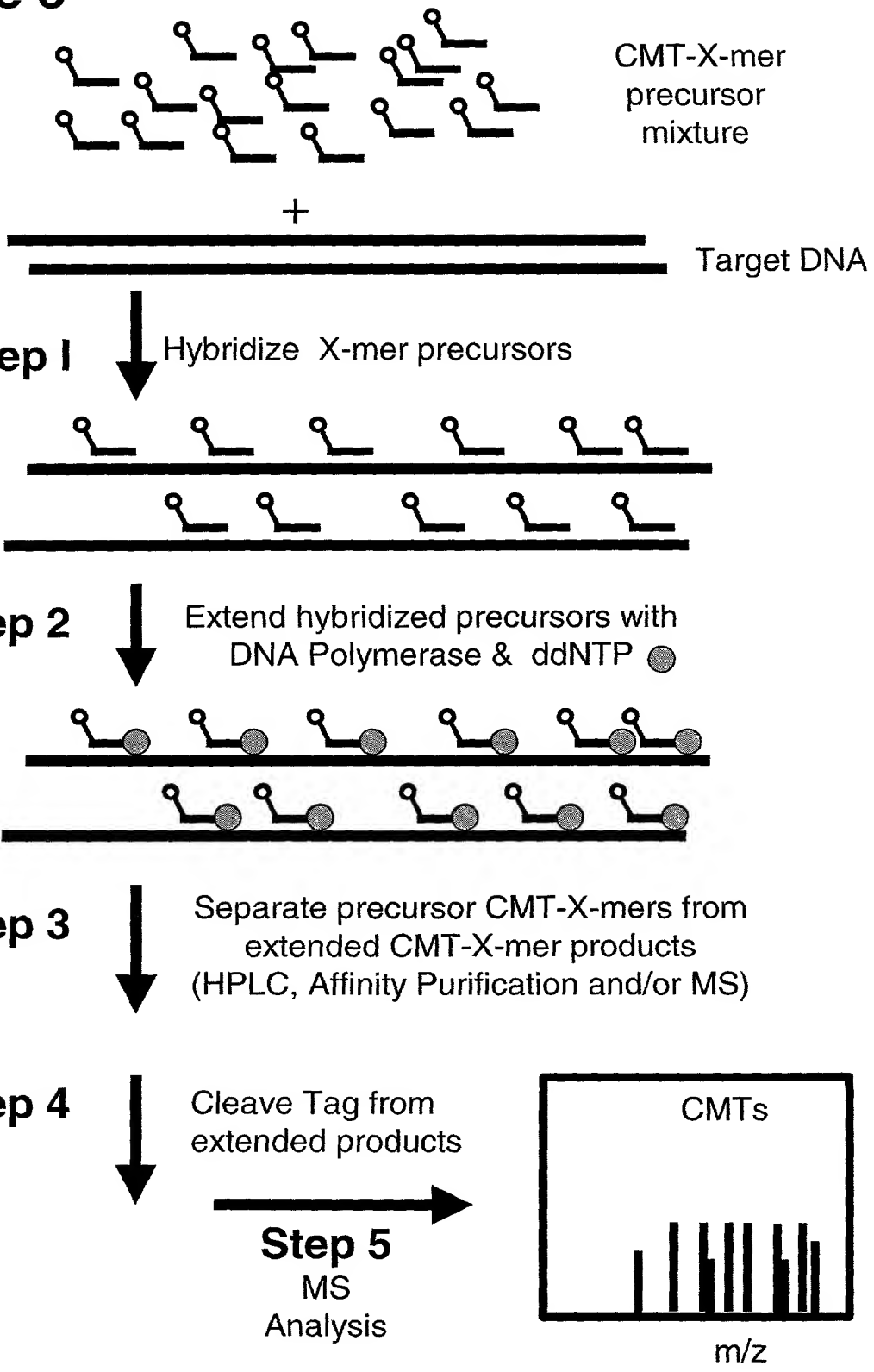

CMT-X-mer
precursor
mixture
+
Target DNA
Step I
Hybridize X-mer precursors
Step 2
Extend hybridized precursors with
DNA Polymerase & ddNTP
Step 3
Separate precursor CMT-X-mers from
extended CMT-X-mer products
(HPLC, Affinity Purification and/or MS)
Step 4
Cleave Tag from
extended products
Step 5
MS
Analysis
CMTs
m/z

Figure 4

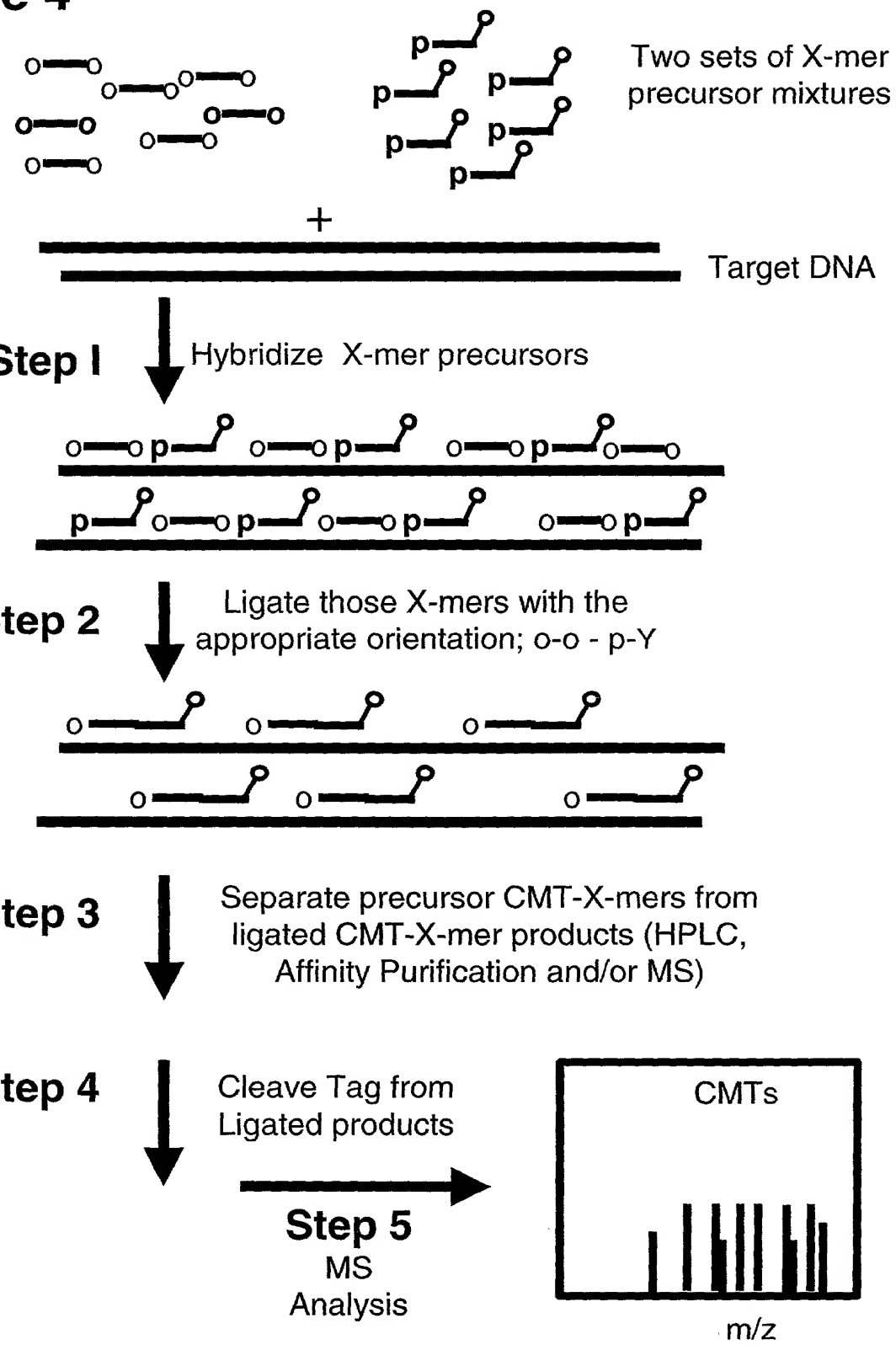

Two sets of X-mer precursor mixtures
+
Target DNA
Step I
Hybridize X-mer precursors
Step 2
Ligate those X-mers with the appropriate orientation; o-o - p-Y
Step 3
Separate precursor CMT-X-mers from ligated CMT-X-mer products (HPLC, Affinity Purification and/or MS)
Step 4
Cleave Tag from Ligated products
Step 5
MS Analysis
CMTs
m/z

Figure 5

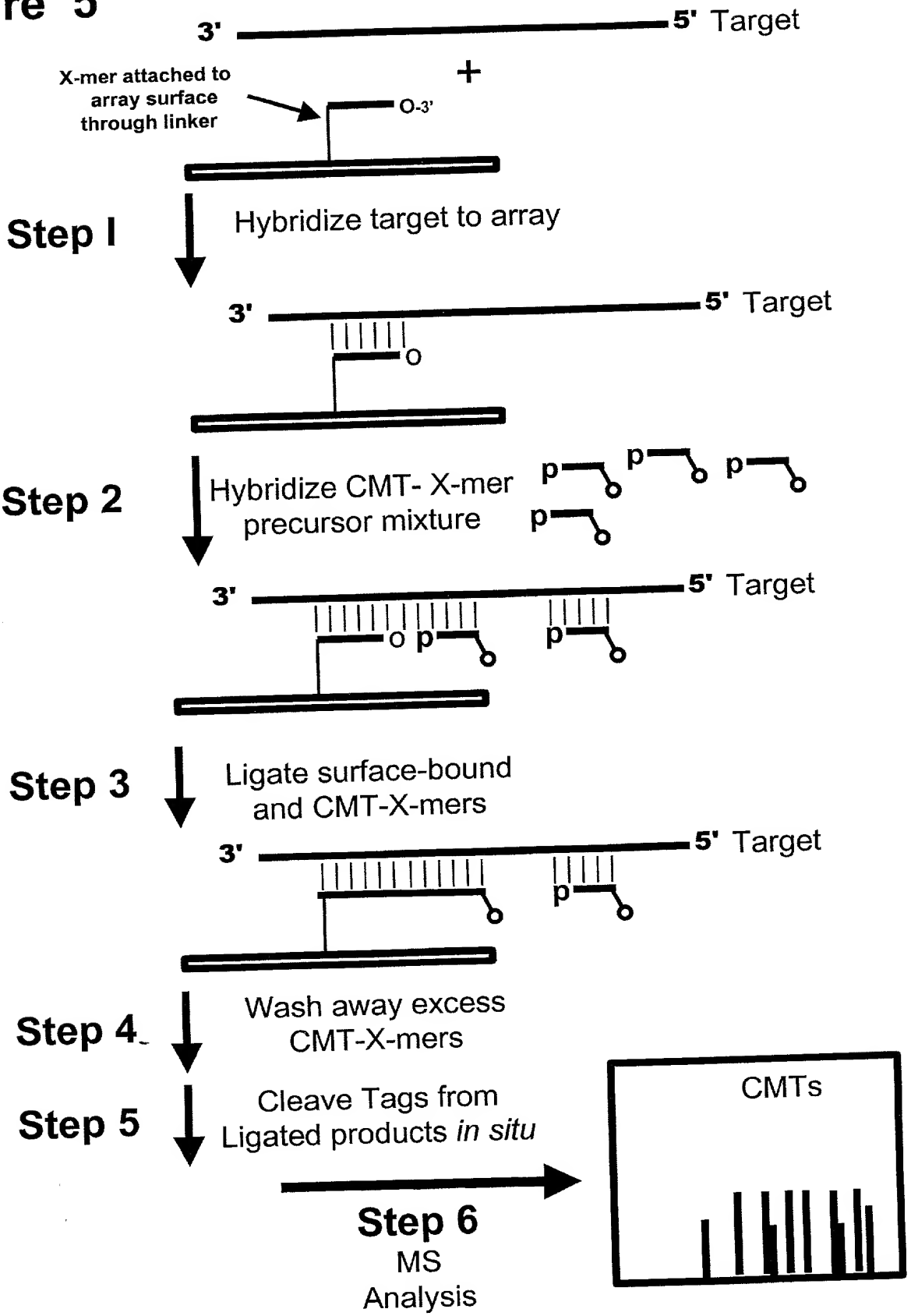

3'
5' Target
X-mer attached to array surface through linker
O-3'
+
Step I
Hybridize target to array
3'
5' Target
o
Step 2
Hybridize CMT- X-mer precursor mixture
p
p
p
p
3'
5' Target
o
p
p
Step 3
Ligate surface-bound and CMT-X-mers
3'
5' Target
p
Step 4
Wash away excess CMT-X-mers
Step 5
Cleave Tags from Ligated products *in situ*
CMTs
Step 6
MS Analysis

Figure 6

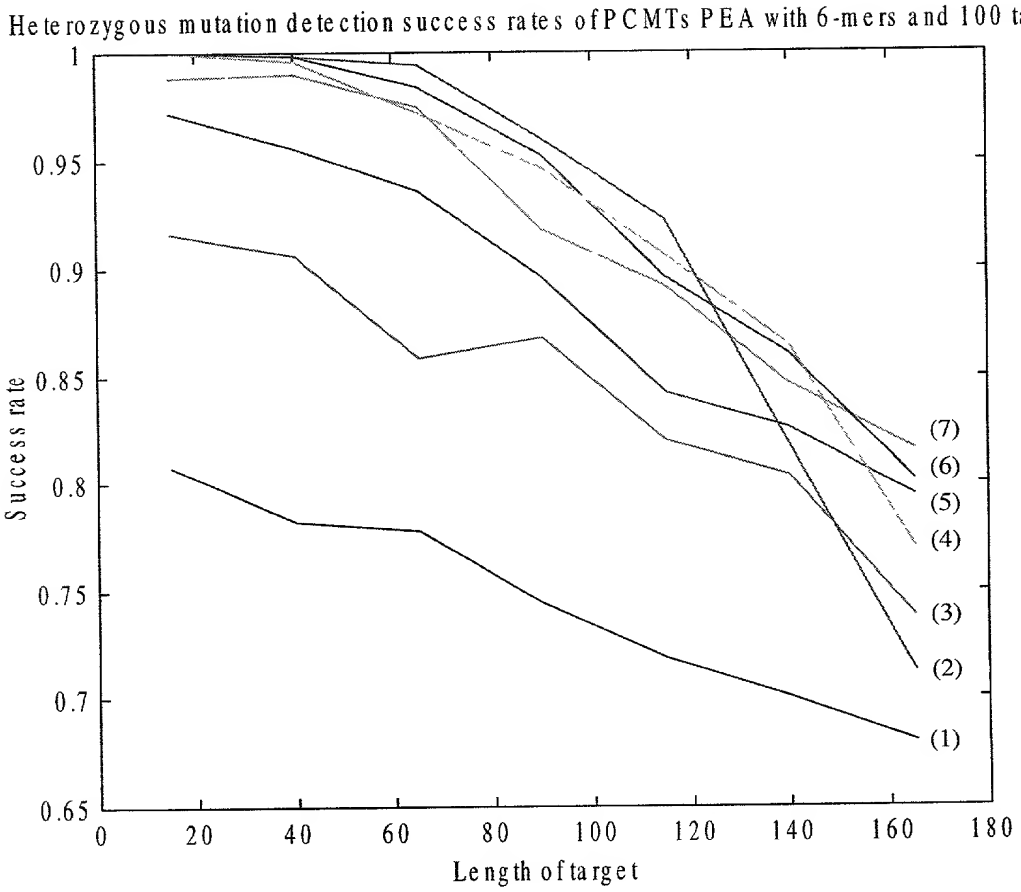

Heterozygous mutation detection success rates of PCMTs PEA with 6-mers and 100 tags
Success rate
1
0.95
0.9
0.85
0.8
0.75
0.7
0.65
0
20
40
60
80
100
120
140
160
180
Length of target
(7)
(6)
(5)
(4)
(3)
(2)
(1)

Figure 7

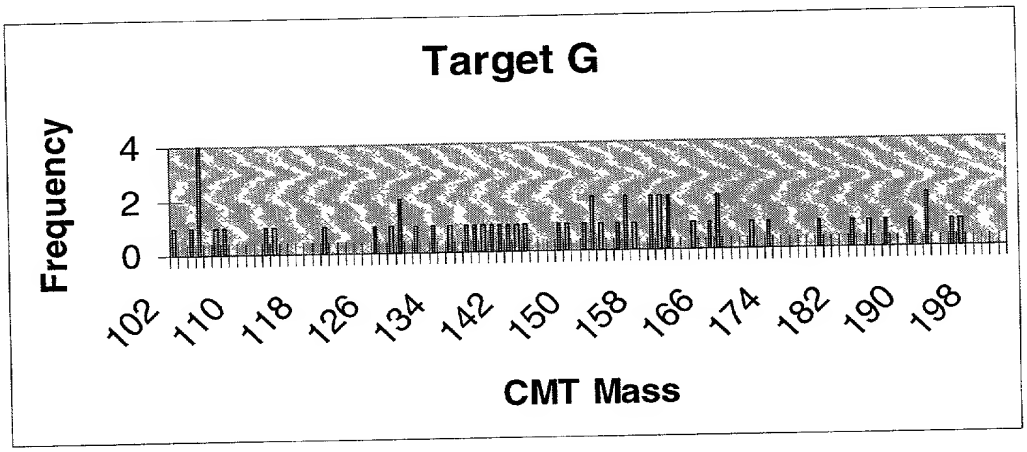
TACACATTGTCAAGGACGTACCCGCCGTACTTGGCCTCCGGGTAGGAGTGGTAGTAGTGTGAC

ATGTGTA
TGTGTAA
GTGTAAC
TGTAACA
GTAACAG
TAACAGT
AACAGTT
ACAGTTC
CAGTTCC
AGTTCCT
GTTCCTG
TTCCTGC
TCCTGCA
CCTGCAT
CTGCATG
TGCATGG
GCATGGG
CATGGGC
ATGGGC**G**
TGGGC**G**G
GGGC**G**GC
GGC**G**GCA
GC**G**GCAT
C**G**GCATG
GGCATGA
GCATGAA
CATGAAC
ATGAACC
TGAACCG
GAACCGG
AACCGGA
ACCGGAG
CCGGAGG
CGGAGGC
GGAGGCC
GAGGCCC
AGGCCCA
GGCCCAT
GCCCATC
CCCATCC
CCATCCT
CATCCTC
ATCCTCA
TCCTCAC
CCTCACC
CTCACCA
TCACCAT
CACCATC
ACCATCA
CCATCAT
CATCATC
ATCATCA
TCATCAC
CATCACA
ATCACAC
TCACACT
CACACTG

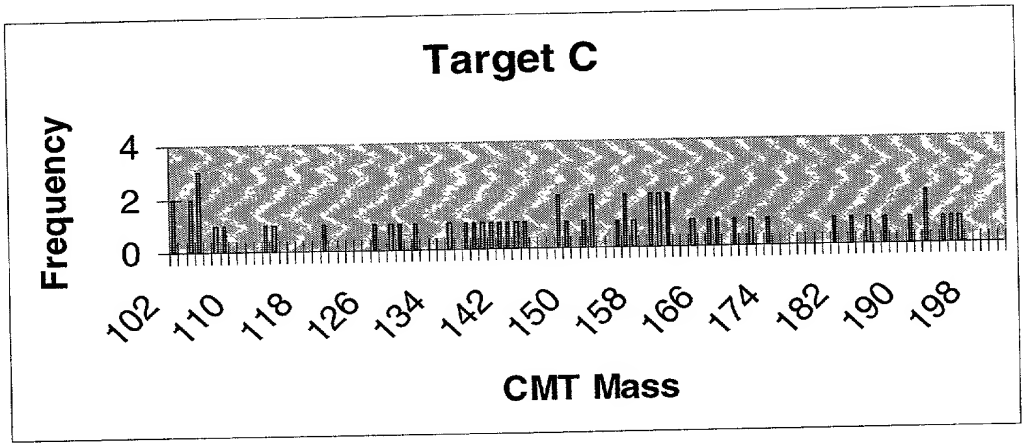
Patent Pending

Figure 8

A


Target G
Frequency
4
2
0
102
110
118
126
134
142
150
158
166
174
182
190
198
CMT Mass

B


Target C
Frequency
4
2
0
102
110
118
126
134
142
150
158
166
174
182
190
198
CMT Mass

C

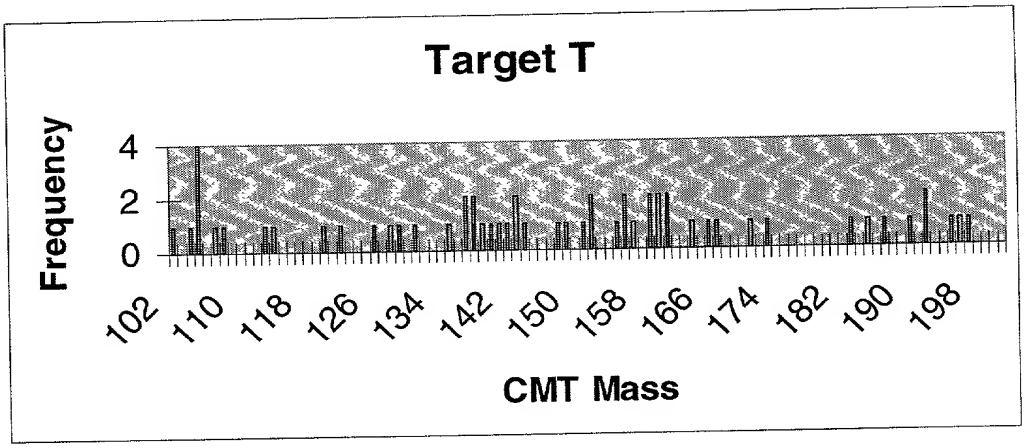
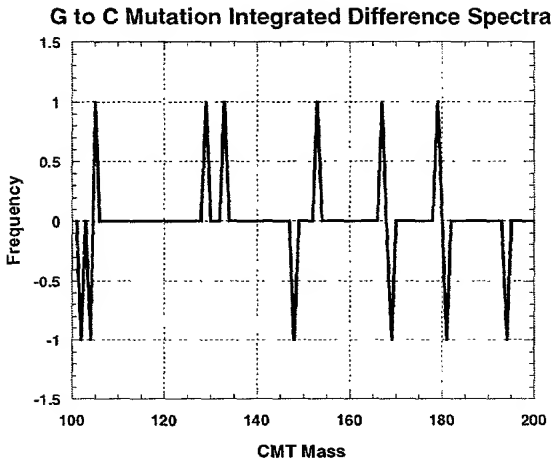
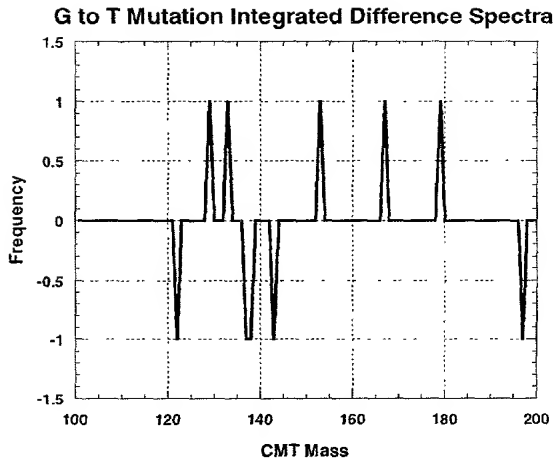

Target T
Frequency
4
2
0
102
110
118
126
134
142
150
158
166
174
182
190
198
CMT Mass

Figure 9

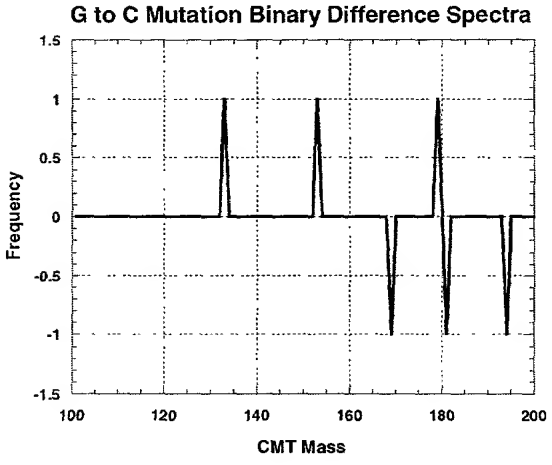
A



B



C



D

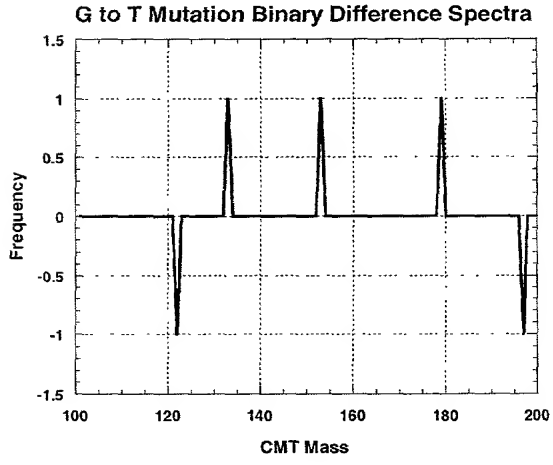
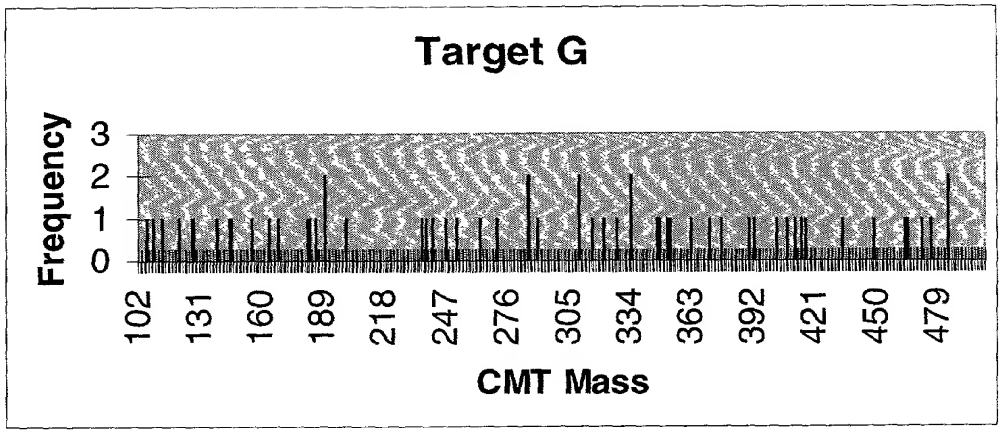
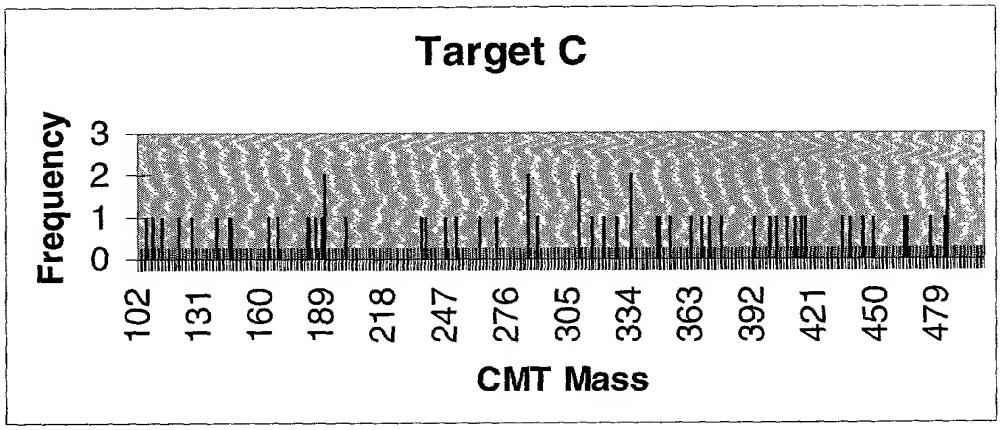


Figure 10

A



B



C

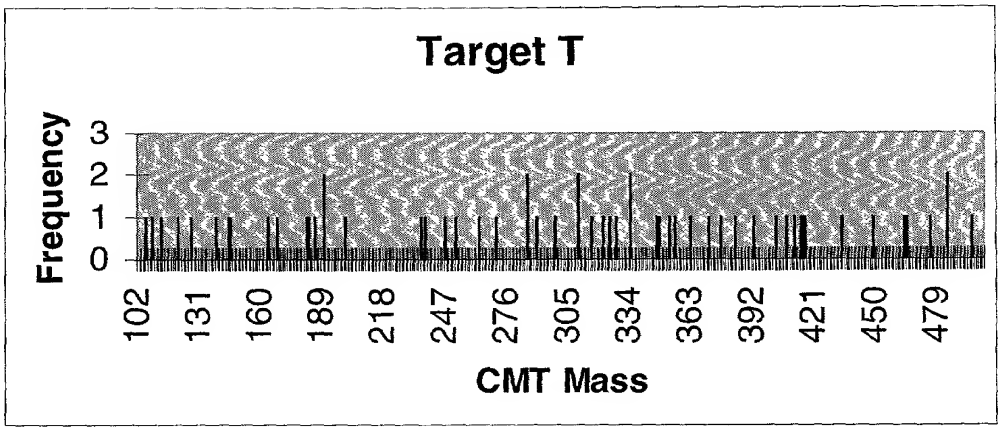
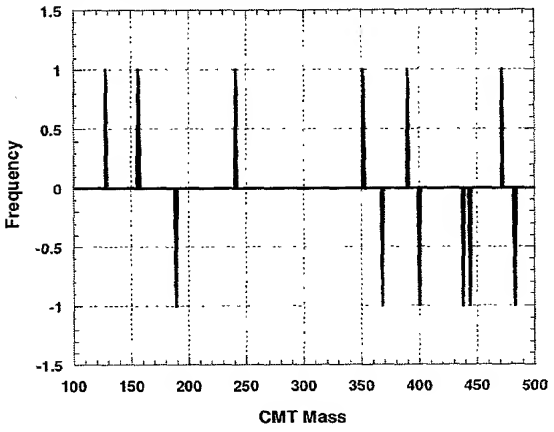
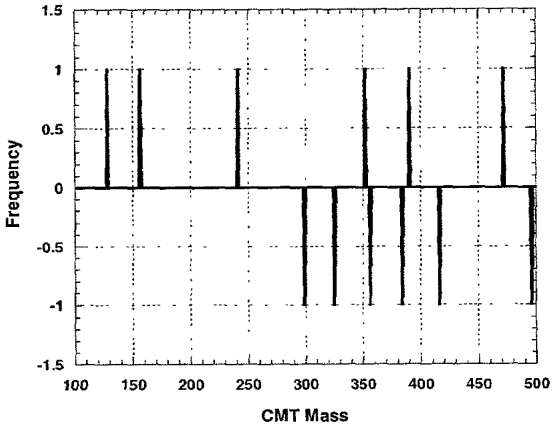


Figure 11

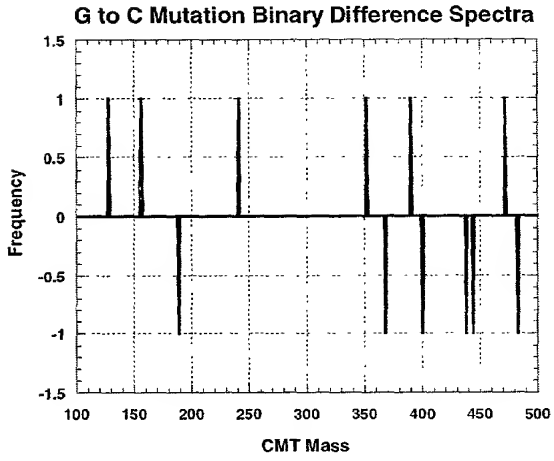
A



B



C



D

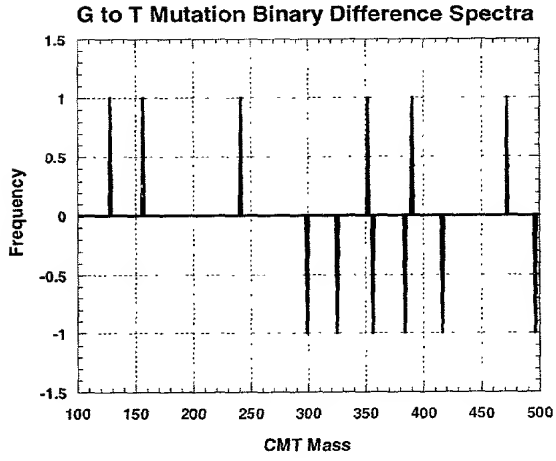
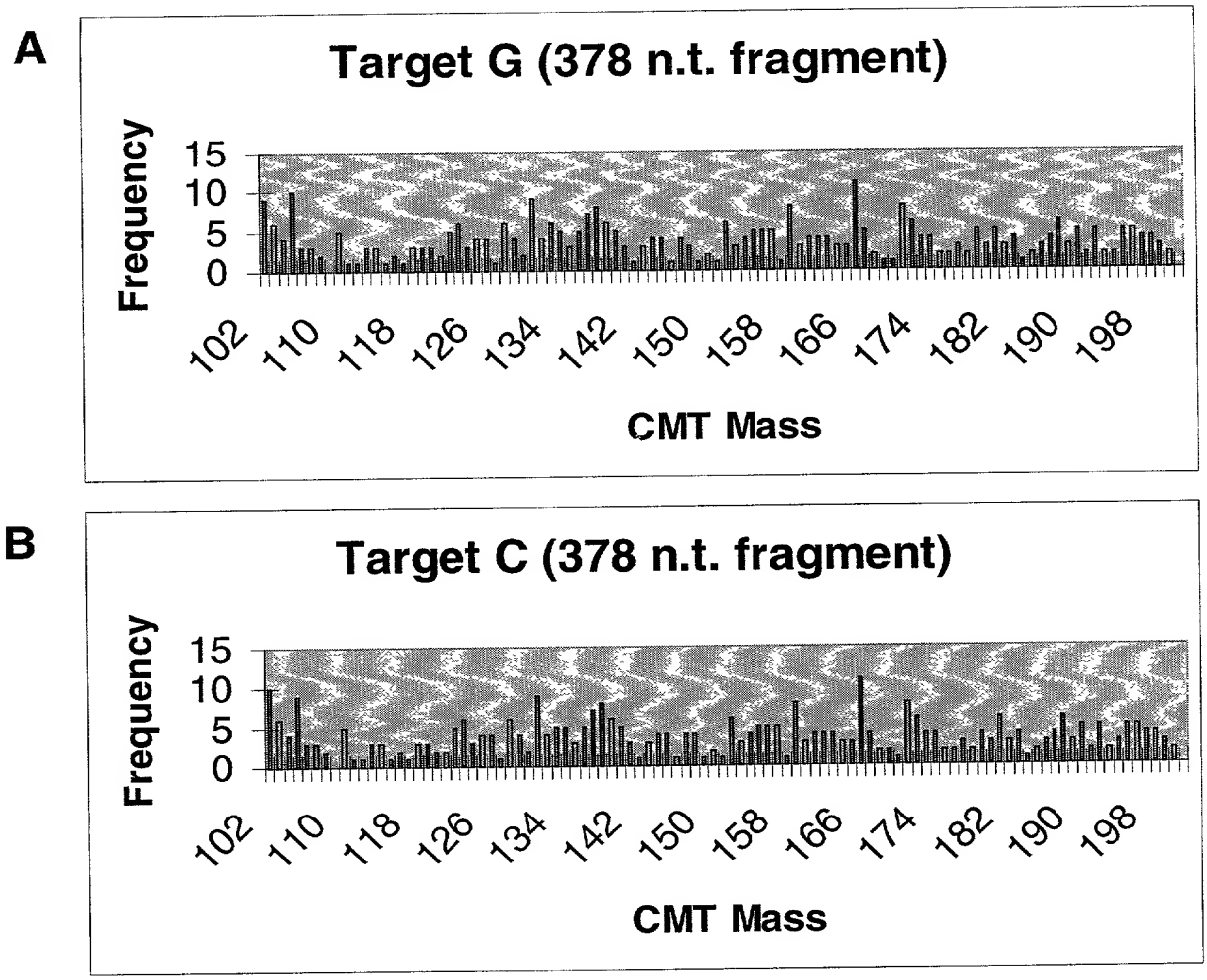
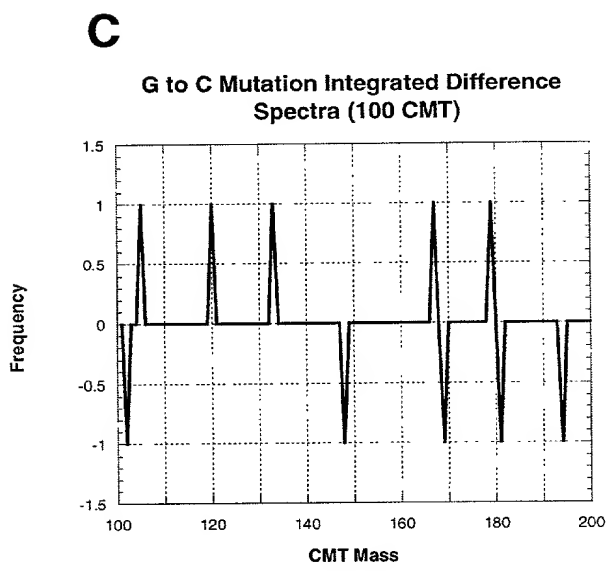


Figure 12


A
Target G (378 n.t. fragment)
Frequency
15
10
5
0
102
110
118
126
134
142
150
158
166
174
182
190
198
CMT Mass
B
Target C (378 n.t. fragment)
Frequency
15
10
5
0
102
110
118
126
134
142
150
158
166
174
182
190
198
CMT Mass


C
G to C Mutation Integrated Difference Spectra (100 CMT)
Frequency
1.5
1
0.5
0
-0.5
-1
-1.5
100
120
140
160
180
200
CMT Mass

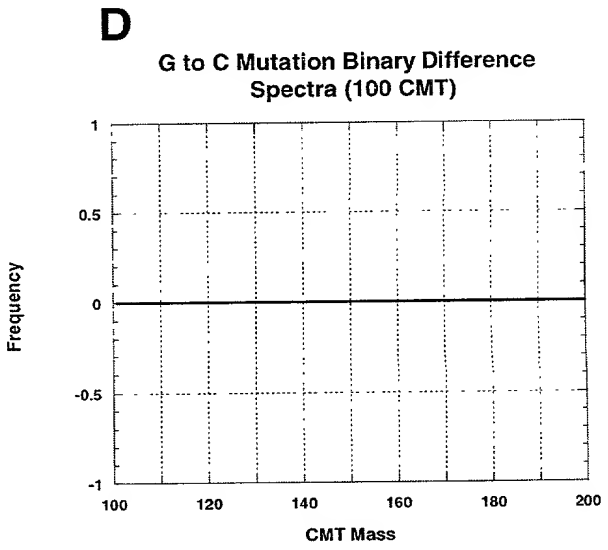
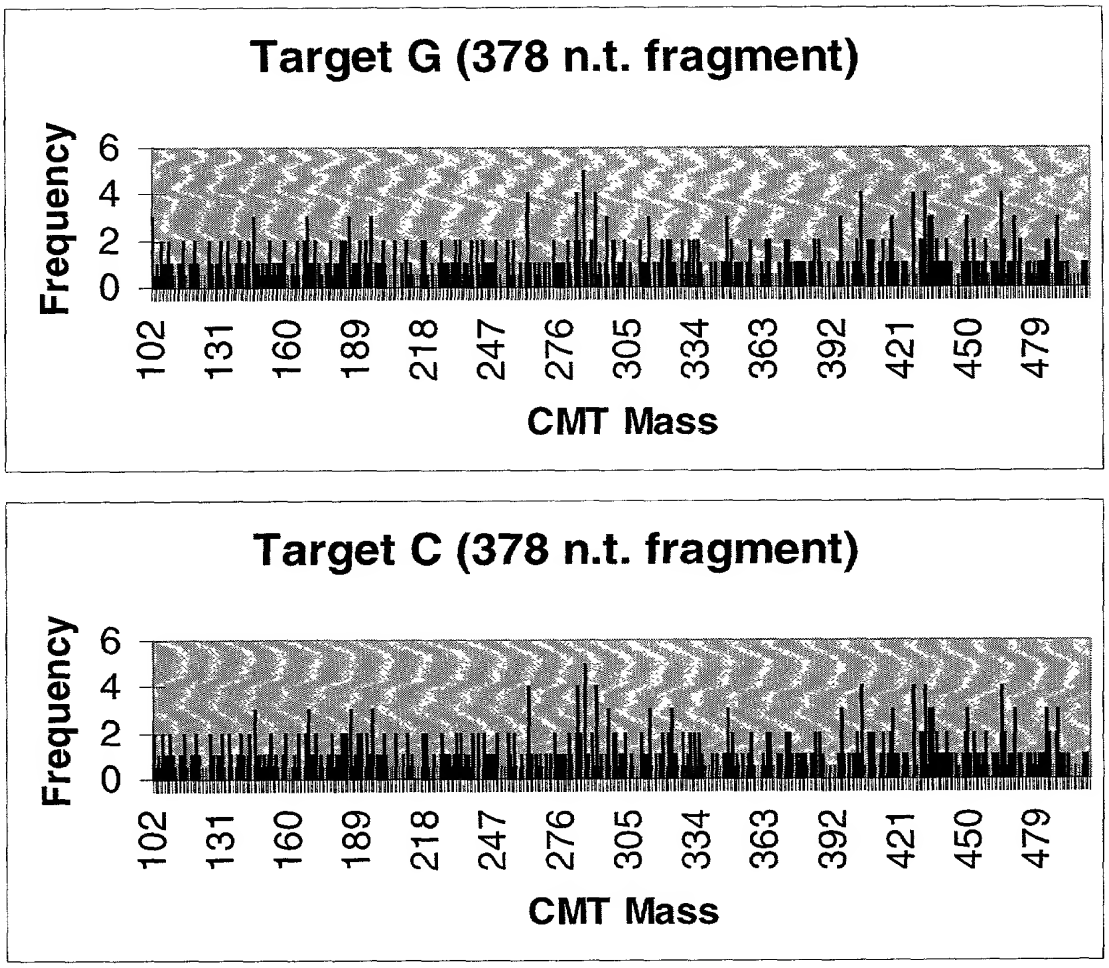
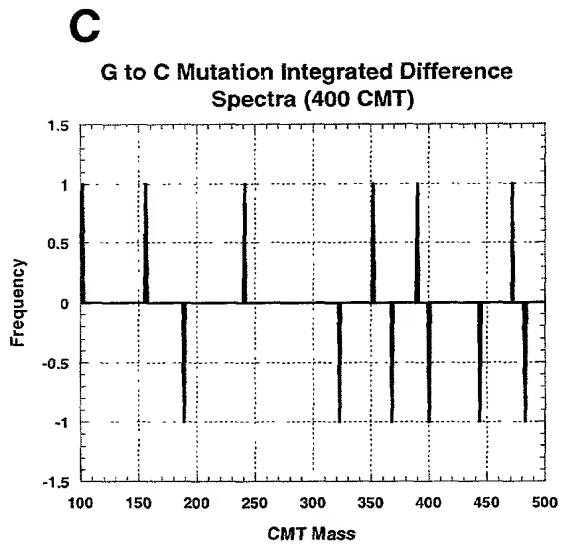
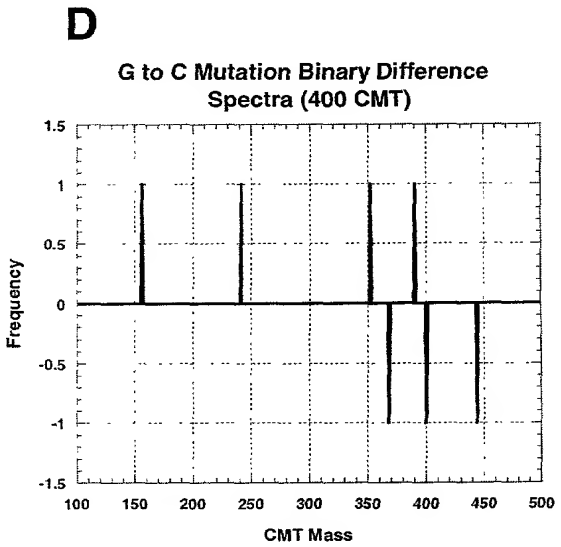

D
G to C Mutation Binary Difference Spectra (100 CMT)
Frequency
1
0.5
0
-0.5
-1
100
120
140
160
180
200
CMT Mass

Figure 13


A
Target G (378 n.t. fragment)
Frequency
6
4
2
0
102
131
160
189
218
247
276
305
334
363
392
421
450
479
CMT Mass
B
Target C (378 n.t. fragment)
Frequency
6
4
2
0
102
131
160
189
218
247
276
305
334
363
392
421
450
479
CMT Mass


C
G to C Mutation Integrated Difference Spectra (400 CMT)
Frequency
1.5
1
0.5
0
-0.5
-1
-1.5
100
150
200
250
300
350
400
450
500
CMT Mass


D
G to C Mutation Binary Difference Spectra (400 CMT)
Frequency
1.5
1
0.5
0
-0.5
-1
-1.5
100
150
200
250
300
350
400
450
500
CMT Mass